



SEQUENCE LISTING

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BERGER, CLAUDIA
LOKEN, CHRISTIANE

<120> HUMAN G-PROTEIN COUPLED RECEPTOR

<130> 01975-0034

<140> 10/088,744

<141> 2002-03-22

<160> 35

<170> PatentIn Ver. 3.2

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<211> 1658

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (55) .. (1299)

<223> IGS4A long version

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| | | | | | | Met | |
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| tca | ggg | atg | gaa | aaa | ctt | cag | 105 |
| Ser | Gly | Met | Glu | Lys | Leu | Gln | |
| | | | 5 | | | 10 | |
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| cta | gaa | gat | cca | ttc | cag | aaa | 153 |
| Leu | Glu | Asp | Pro | Phe | Gln | Lys | |
| | | | 20 | | | 25 | |
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| gcc | ttc | ctc | tgc | gga | cct | cgg | 201 |
| Ala | Phe | Leu | Cys | Gly | Pro | Arg | |
| | | | | | | 40 | |
| | | | | | | 45 | |
| gtg | gtg | tat | gtg | cca | att | ttt | 249 |
| Val | Val | Tyr | Val | Pro | Ile | Phe | |
| | | | | | | 55 | |
| | | | | | | 60 | |
| gtg | tgc | ctg | gtg | att | ctg | cag | 297 |
| Val | Cys | Leu | Val | Ile | Leu | Gln | |
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| | | | | | | 75 | |
| | | | | | | 80 | |

| | |
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| tac tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt | 345 |
| Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu | |
| 85 90 95 | |
| gga atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg | 393 |
| Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu | |
| 100 105 110 | |
| ttc ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg | 441 |
| Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val | |
| 115 120 125 | |
| tgc ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac | 489 |
| Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr | |
| 130 135 140 145 | |
| gtg gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc | 537 |
| Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg | |
| 150 155 160 | |
| cgg gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc | 585 |
| Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe | |
| 165 170 175 | |
| tcc ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc | 633 |
| Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro | |
| 180 185 190 | |
| aat ggg tcc ctg gtc cca ggt tgc gcc acc tgt acg gtc atc aag ccc | 681 |
| Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro | |
| 195 200 205 | |
| atg tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac | 729 |
| Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr | |
| 210 215 220 225 | |
| ctc ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc | 777 |
| Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu | |
| 230 235 240 | |
| aga cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat | 825 |
| Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn | |
| 245 250 255 | |
| att caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg | 873 |
| Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu | |
| 260 265 270 | |
| gtc tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc | 921 |
| Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu | |
| 275 280 285 | |

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ttc ttc agc ttt gtg gag gag tgg agt gaa tcc ctg gct gct gtg ttc 969
Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val Phe
290                295                300                305

aac ctc gtc cat gtg gtg tca ggt gtc ttc ttc tac ctg agc tca gct 1017
Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser Ala
310                315                320

gtc aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca 1065
Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala
325                330                335

ttc cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat 1113
Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His
340                345                350

gac cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc 1161
Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys
355                360                365

cac ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cca tgt cag 1209
His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys Gln
370                375                380                385

tca tcc atg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag 1257
Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln
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atg tca aga aca aac tat caa agc ttc cac ttt aac aaa acc 1299
Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr
405                410                415

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aatgtatgcc ttctcatatg atattagaga ggtagaatgg ctcttacaac tcatgtaccc 1419

attgctagtt tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac 1479

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 Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val
 50 55 60
 Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr
 65 70 75 80
 Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu
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 Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe
 100 105 110
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 Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg
 130 135 140
 Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg
 145 150 155 160
 Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu
 165 170 175
 Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe
 180 185 190
 Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys
 195 200 205
 Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe
 210 215 220
 Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala
 225 230 235 240
 Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala
 245 250 255
 Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val
 260 265 270
 Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg
 275 280 285
 Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val
 290 295 300

Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser
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Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala
325 330 335

Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln
340 345 350

His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu
355 360 365

Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys
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Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu
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Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu
1 5 10 15

gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156
Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala
20 25 30

ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct gtg 204
Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val
35 40 45

gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg gtg 252
Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val
50 55 60

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|---|-----|
| tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac tac | 300 |
| Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr | |
| 65 70 75 | |
| tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt gga | 348 |
| Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly | |
| 80 85 90 95 | |
| atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg ttc | 396 |
| Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe | |
| 100 105 110 | |
| ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg tgc | 444 |
| Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys | |
| 115 120 125 | |
| ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac gtg | 492 |
| Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val | |
| 130 135 140 | |
| gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc cgg | 540 |
| Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg | |
| 145 150 155 | |
| gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc tcc | 588 |
| Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser | |
| 160 165 170 175 | |
| ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc aat | 636 |
| Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn | |
| 180 185 190 | |
| ggg tcc ctg gtc cca ggt tgc gcc acc tgt acg gtc atc aag ccc atg | 684 |
| Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met | |
| 195 200 205 | |
| tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac ctc | 732 |
| Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu | |
| 210 215 220 | |
| ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc aga | 780 |
| Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg | |
| 225 230 235 | |
| cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat att | 828 |
| Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile | |
| 240 245 250 255 | |
| caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg gtc | 876 |
| Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu Val | |
| 260 265 270 | |

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| tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc ttc | 924 |
| Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu Phe | |
| 275 280 285 | |
| ttc agc ttt gtg gag gag tgg agt gaa tcc ctg gct gct gtg ttc aac | 972 |
| Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val Phe Asn | |
| 290 295 300 | |
| ctc gtc cat gtg gtg tca ggt gtc ttc ttc tac ctg agc tca gct gtc | 1020 |
| Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser Ala Val | |
| 305 310 315 | |
| aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca ttc | 1068 |
| Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala Phe | |
| 320 325 330 335 | |
| cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat gac | 1116 |
| Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His Asp | |
| 340 345 350 | |
| cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc cac | 1164 |
| Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys His | |
| 355 360 365 | |
| ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cca tgt cag tca | 1212 |
| Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys Gln Ser | |
| 370 375 380 | |
| tcc atg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag atg | 1260 |
| Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln Met | |
| 385 390 395 | |
| tca aga aca aac tat caa agc ttc cac ttt aac aaa acc tgaattcttt | 1309 |
| Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr | |
| 400 405 410 | |
| cagagctgac tctcctctat gcctcaaaac ttcagagagg aacatcccat aatgtatgcc | 1369 |
| ttctcatatg atattagaga ggtagaatgg ctcttacaac tcatgtaccc attgctagtt | 1429 |
| tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac ccaagactgc | 1489 |
| ctgatttttta gttatctttc cactatccta actgcctcat gccctttcac tagttcatgc | 1549 |
| caagaacgtg actggaaagg catggcacct ataccttgat taatttccat taatggaaat | 1609 |
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| Met | Glu | Lys | Leu | Gln | Asn | Ala | Ser | Trp | Ile | Tyr | Gln | Gln | Lys | Leu | Glu | 1 | 5 | 10 | 15 |
| Asp | Pro | Phe | Gln | Lys | His | Leu | Asn | Ser | Thr | Glu | Glu | Tyr | Leu | Ala | Phe | 20 | 25 | 30 | |
| Leu | Cys | Gly | Pro | Arg | Arg | Ser | His | Phe | Phe | Leu | Pro | Val | Ser | Val | Val | 35 | 40 | 45 | |
| Tyr | Val | Pro | Ile | Phe | Val | Val | Gly | Val | Ile | Gly | Asn | Val | Leu | Val | Cys | 50 | 55 | 60 | |
| Leu | Val | Ile | Leu | Gln | His | Gln | Ala | Met | Lys | Thr | Pro | Thr | Asn | Tyr | Tyr | 65 | 70 | 75 | 80 |
| Leu | Phe | Ser | Leu | Ala | Val | Ser | Asp | Leu | Leu | Val | Leu | Leu | Leu | Gly | Met | 85 | 90 | 95 | |
| Pro | Leu | Glu | Val | Tyr | Glu | Met | Trp | Arg | Asn | Tyr | Pro | Phe | Leu | Phe | Gly | 100 | 105 | 110 | |
| Pro | Val | Gly | Cys | Tyr | Phe | Lys | Thr | Ala | Leu | Phe | Glu | Thr | Val | Cys | Phe | 115 | 120 | 125 | |
| Ala | Ser | Ile | Leu | Ser | Ile | Thr | Thr | Val | Ser | Val | Glu | Arg | Tyr | Val | Ala | 130 | 135 | 140 | |
| Ile | Leu | His | Pro | Phe | Arg | Ala | Lys | Leu | Gln | Ser | Thr | Arg | Arg | Arg | Ala | 145 | 150 | 155 | 160 |
| Leu | Arg | Ile | Leu | Gly | Ile | Val | Trp | Gly | Phe | Ser | Val | Leu | Phe | Ser | Leu | 165 | 170 | 175 | |
| Pro | Asn | Thr | Ser | Ile | His | Gly | Ile | Lys | Phe | His | Tyr | Phe | Pro | Asn | Gly | 180 | 185 | 190 | |
| Ser | Leu | Val | Pro | Gly | Ser | Ala | Thr | Cys | Thr | Val | Ile | Lys | Pro | Met | Trp | 195 | 200 | 205 | |
| Ile | Tyr | Asn | Phe | Ile | Ile | Gln | Val | Thr | Ser | Phe | Leu | Phe | Tyr | Leu | Leu | 210 | 215 | 220 | |
| Pro | Met | Thr | Val | Ile | Ser | Val | Leu | Tyr | Tyr | Leu | Met | Ala | Leu | Arg | Leu | 225 | 230 | 235 | 240 |
| Lys | Lys | Asp | Lys | Ser | Leu | Glu | Ala | Asp | Glu | Gly | Asn | Ala | Asn | Ile | Gln | 245 | 250 | 255 | |
| Arg | Pro | Cys | Arg | Lys | Ser | Val | Asn | Lys | Met | Leu | Phe | Val | Leu | Val | Leu | 260 | 265 | 270 | |
| Val | Phe | Ala | Ile | Cys | Trp | Ala | Pro | Phe | His | Ile | Asp | Arg | Leu | Phe | Phe | 275 | 280 | 285 | |

Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val Phe Asn Leu
 290 295 300
 Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser Ala Val Asn
 305 310 315 320
 Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala Phe Gln
 325 330 335
 Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His Asp Pro
 340 345 350
 Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys His Phe
 355 360 365
 Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys Gln Ser Ser
 370 375 380
 Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln Met Ser
 385 390 395 400
 Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr
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 <223> IGS4B long version

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 Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys
 5 10 15
 cta gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg 153
 Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu
 20 25 30
 gcc ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct 201
 Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser
 35 40 45

| | |
|---|-----|
| gtg gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg | 249 |
| Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu | |
| 50 55 60 65 | |
| gtg tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac | 297 |
| Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn | |
| 70 75 80 | |
| tac tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt | 345 |
| Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu | |
| 85 90 95 | |
| gga atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg | 393 |
| Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu | |
| 100 105 110 | |
| ttc ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg | 441 |
| Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val | |
| 115 120 125 | |
| tgc ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac | 489 |
| Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr | |
| 130 135 140 145 | |
| gtg gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc | 537 |
| Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg | |
| 150 155 160 | |
| cgg gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc | 585 |
| Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe | |
| 165 170 175 | |
| tcc ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc | 633 |
| Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro | |
| 180 185 190 | |
| aat ggg tcc ctg gtc cca ggt tcg gcc acc tgt acg gtc atc aag ccc | 681 |
| Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro | |
| 195 200 205 | |
| atg tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac | 729 |
| Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr | |
| 210 215 220 225 | |
| ctc ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc | 777 |
| Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu | |
| 230 235 240 | |
| aga cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat | 825 |
| Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn | |
| 245 250 255 | |

| | |
|---|------|
| att caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg | 873 |
| Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu | |
| 260 265 270 | |
| gtc tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc | 921 |
| Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu | |
| 275 280 285 | |
| ttc ttc agc ttt gtg gag gag tgg act gaa tcc ctg gct gct gtg ttc | 969 |
| Phe Phe Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val Phe | |
| 290 295 300 305 | |
| aac ctc gtc cat gtg gtg tca ggt gtc tta ttc tac ctg agc tca gct | 1017 |
| Asn Leu Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser Ala | |
| 310 315 320 | |
| gtc aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca | 1065 |
| Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala | |
| 325 330 335 | |
| ttc cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat | 1113 |
| Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His | |
| 340 345 350 | |
| gac cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc | 1161 |
| Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys | |
| 355 360 365 | |
| cac ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cta tgt cag | 1209 |
| His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys Gln | |
| 370 375 380 385 | |
| tca tcc gtg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag | 1257 |
| Ser Ser Val His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln | |
| 390 395 400 | |
| atg tca aga aca aac tat caa agc ttc cac ttt aac aaa acc | 1299 |
| Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr | |
| 405 410 415 | |
| tgaattcttt cagagctgac tctcctctat gcctcaaaac ttcagagagg aacatcccat | 1359 |
| aatgtatgcc ttctcatatg aaattagaga ggtagaatgg ctcttacaac tcatgtaccc | 1419 |
| attgctagtt tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac | 1479 |
| ccaagactgc ctgattttta gttatctttc cactatccta actgcctcat gcccttcac | 1539 |
| tagttcatgc caagaacgtg actggaaagg catggcacct ataccttgat taatttccat | 1599 |
| taatggaaat gggtcgtcct gagtcatcta cgttccgagt caggctgtca ctctacta | 1658 |

<210> 6
 <211> 415
 <212> PRT
 <213> Homo sapiens

<400> 6

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gly | Met | Glu | Lys | Leu | Gln | Asn | Ala | Ser | Trp | Ile | Tyr | Gln | Gln |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys | Leu | Glu | Asp | Pro | Phe | Gln | Lys | His | Leu | Asn | Ser | Thr | Glu | Glu | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Ala | Phe | Leu | Cys | Gly | Pro | Arg | Arg | Ser | His | Phe | Phe | Leu | Pro | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Val | Val | Tyr | Val | Pro | Ile | Phe | Val | Val | Gly | Val | Ile | Gly | Asn | Val |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Val | Cys | Leu | Val | Ile | Leu | Gln | His | Gln | Ala | Met | Lys | Thr | Pro | Thr |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 |
| Asn | Tyr | Tyr | Leu | Phe | Ser | Leu | Ala | Val | Ser | Asp | Leu | Leu | Val | Leu | Leu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Leu | Gly | Met | Pro | Leu | Glu | Val | Tyr | Glu | Met | Trp | Arg | Asn | Tyr | Pro | Phe |
| | | 100 | | | | | | 105 | | | | | 110 | | |
| Leu | Phe | Gly | Pro | Val | Gly | Cys | Tyr | Phe | Lys | Thr | Ala | Leu | Phe | Glu | Thr |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Val | Cys | Phe | Ala | Ser | Ile | Leu | Ser | Ile | Thr | Thr | Val | Ser | Val | Glu | Arg |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Tyr | Val | Ala | Ile | Leu | His | Pro | Phe | Arg | Ala | Lys | Leu | Gln | Ser | Thr | Arg |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Arg | Arg | Ala | Leu | Arg | Ile | Leu | Gly | Ile | Val | Trp | Gly | Phe | Ser | Val | Leu |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Phe | Ser | Leu | Pro | Asn | Thr | Ser | Ile | His | Gly | Ile | Lys | Phe | His | Tyr | Phe |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Pro | Asn | Gly | Ser | Leu | Val | Pro | Gly | Ser | Ala | Thr | Cys | Thr | Val | Ile | Lys |
| | | 195 | | | | 200 | | | | | | 205 | | | |
| Pro | Met | Trp | Ile | Tyr | Asn | Phe | Ile | Ile | Gln | Val | Thr | Ser | Phe | Leu | Phe |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Tyr | Leu | Leu | Pro | Met | Thr | Val | Ile | Ser | Val | Leu | Tyr | Tyr | Leu | Met | Ala |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Leu | Arg | Leu | Lys | Lys | Asp | Lys | Ser | Leu | Glu | Ala | Asp | Glu | Gly | Asn | Ala |
| | | | | 245 | | | | | 250 | | | | | 255 | |

Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val
 260 265 270
 Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg
 275 280 285
 Leu Phe Phe Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val
 290 295 300
 Phe Asn Leu Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser
 305 310 315 320
 Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala
 325 330 335
 Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln
 340 345 350
 His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu
 355 360 365
 Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys
 370 375 380
 Gln Ser Ser Val His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu
 385 390 395 400
 Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr
 405 410 415

<210> 7

<211> 1658

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (64)..(1299)

<223> IGS4B short version

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 ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa cta 108
 Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu
 1 5 10 15
 gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156
 Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala
 20 25 30

| | |
|---|-----|
| ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct gtg | 204 |
| Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val | |
| 35 40 45 | |
| gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg gtg | 252 |
| Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val | |
| 50 55 60 | |
| tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac tac | 300 |
| Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr | |
| 65 70 75 | |
| tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt gga | 348 |
| Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly | |
| 80 85 90 95 | |
| atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg ttc | 396 |
| Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe | |
| 100 105 110 | |
| ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg tgc | 444 |
| Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys | |
| 115 120 125 | |
| ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac gtg | 492 |
| Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val | |
| 130 135 140 | |
| gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc cgg | 540 |
| Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg | |
| 145 150 155 | |
| gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc tcc | 588 |
| Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser | |
| 160 165 170 175 | |
| ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc aat | 636 |
| Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn | |
| 180 185 190 | |
| ggg tcc ctg gtc cca ggt tgc gcc acc tgt acg gtc atc aag ccc atg | 684 |
| Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met | |
| 195 200 205 | |
| tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac ctc | 732 |
| Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu | |
| 210 215 220 | |
| ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc aga | 780 |
| Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg | |
| 225 230 235 | |

| | |
|---|------|
| cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat att | 828 |
| Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile | |
| 240 245 250 255 | |
| caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg gtc | 876 |
| Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu Val | |
| 260 265 270 | |
| tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc ttc | 924 |
| Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu Phe | |
| 275 280 285 | |
| ttc agc ttt gtg gag gag tgg act gaa tcc ctg gct gct gtg ttc aac | 972 |
| Phe Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val Phe Asn | |
| 290 295 300 | |
| ctc gtc cat gtg gtg tca ggt gtc tta ttc tac ctg agc tca gct gtc | 1020 |
| Leu Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser Ala Val | |
| 305 310 315 | |
| aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca ttc | 1068 |
| Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala Phe | |
| 320 325 330 335 | |
| cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat gac | 1116 |
| Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His Asp | |
| 340 345 350 | |
| cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc cac | 1164 |
| Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys His | |
| 355 360 365 | |
| ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cta tgt cag tca | 1212 |
| Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys Gln Ser | |
| 370 375 380 | |
| tcc gtg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag atg | 1260 |
| Ser Val His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln Met | |
| 385 390 395 | |
| tca aga aca aac tat caa agc ttc cac ttt aac aaa acc tgaattcttt | 1309 |
| Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr | |
| 400 405 410 | |
| cagagctgac tctcctctat gcctcaaaac ttcagagagg aacatcccat aatgtatgcc | 1369 |
| ttctcatatg aaattagaga ggtagaatgg ctcttacaac tcatgtaccc attgctagtt | 1429 |
| tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac ccaagactgc | 1489 |
| ctgattttta gttatctttc cactataccta actgcctcat gcccttcac tagttcatgc | 1549 |
| caagaacgtg actggaaagg catggcacct ataccttgat taatttccat taatggaaat | 1609 |

ggttcgctct gagtcaccta cgttccgagt caggctgtca ctcctacta

1658

<210> 8

<211> 412

<212> PRT

<213> Homo sapiens

<400> 8

Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu Glu
 1 5 10 15

Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala Phe
 20 25 30

Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val Val
 35 40 45

Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val Cys
 50 55 60

Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr Tyr
 65 70 75 80

Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly Met
 85 90 95

Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe Gly
 100 105 110

Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys Phe
 115 120 125

Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val Ala
 130 135 140

Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg Ala
 145 150 155 160

Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser Leu
 165 170 175

Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn Gly
 180 185 190

Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met Trp
 195 200 205

Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu Leu
 210 215 220

Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg Leu
 225 230 235 240


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<220>
<221> CDS
<222> (55)..(942)
<223> IGS4A truncated DNA long version
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<400> 9
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                                         Met
                                         1

tca ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa 105
Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys
          5              10              15

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| | |
|---|-----|
| cta gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg | 153 |
| Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu | |
| 20 25 30 | |
| gcc ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct | 201 |
| Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser | |
| 35 40 45 | |
| gtg gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg | 249 |
| Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu | |
| 50 55 60 65 | |
| gtg tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac | 297 |
| Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn | |
| 70 75 80 | |
| tac tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt | 345 |
| Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu | |
| 85 90 95 | |
| gga atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg | 393 |
| Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu | |
| 100 105 110 | |
| ttc ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg | 441 |
| Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val | |
| 115 120 125 | |
| tgc ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac | 489 |
| Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr | |
| 130 135 140 145 | |
| gtg gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc | 537 |
| Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg | |
| 150 155 160 | |
| cgg gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc | 585 |
| Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe | |
| 165 170 175 | |
| tcc ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc | 633 |
| Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro | |
| 180 185 190 | |
| aat ggg tcc ctg gtc cca ggt tgc gcc acc tgt acg gtc atc aag ccc | 681 |
| Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro | |
| 195 200 205 | |
| atg tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac | 729 |
| Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr | |
| 210 215 220 225 | |

[illegible]

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<210> 10
<211> 296
<212> PRT
<213> Homo sapiens
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Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr
      20              25              30

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Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val
 35 40 45
 Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val
 50 55 60
 Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr
 65 70 75 80
 Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu
 85 90 95
 Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe
 100 105 110
 Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr
 115 120 125
 Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg
 130 135 140
 Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg
 145 150 155 160
 Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu
 165 170 175
 Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe
 180 185 190
 Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys
 195 200 205
 Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe
 210 215 220
 Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala
 225 230 235 240
 Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala
 245 250 255
 Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu
 260 265 270
 Trp Arg Ser Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met
 275 280 285
 Trp Cys Gln Val Ser Ser Ser Thr
 290 295

<210> 11
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (64)..(942)
 <223> IGS4A truncated DNA short version

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 ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa cta 108
 Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu
 1 5 10 15
 gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156
 Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala
 20 25 30
 ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct gtg 204
 Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val
 35 40 45
 gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg gtg 252
 Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val
 50 55 60
 tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac tac 300
 Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr
 65 70 75
 tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt gga 348
 Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly
 80 85 90 95
 atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg ttc 396
 Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe
 100 105 110
 ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg tgc 444
 Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys
 115 120 125
 ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac gtg 492
 Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val
 130 135 140
 gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc cgg 540
 Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg
 145 150 155

gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc tcc 588
 Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser
 160 165 170 175

ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc aat 636
 Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn
 180 185 190

ggg tcc ctg gtc cca ggt tgg gcc acc tgt acg gtc atc aag ccc atg 684
 Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met
 195 200 205

tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac ctc 732
 Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu
 210 215 220

ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc aga 780
 Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg
 225 230 235

cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat att 828
 Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile
 240 245 250 255

caa aga ccc tgc aga aaa tca gtc aac aag atg ctg tct ttg tgg agg 876
 Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu Trp Arg
 260 265 270

agt gga gtg aat ccc tgg ctg ctg tgt tca acc tgg tcc atg tgg tgt 924
 Ser Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met Trp Cys
 275 280 285

cag gtg tct tct tct acc tgagctcagc tgtcaacccc attatctata 972
 Gln Val Ser Ser Ser Thr
 290

acctactgtc tcgccgcttc caggcagcat tccagaatgt gatctcttct ttccacaaac 1032

agtggcactc ccagcatgac ccacagttgc cacctgccca gcggaacatc ttcttgacag 1092

aatgccactt tgtggagctg accgaagata taggtcccca attcccatgt cagtcaccca 1152

tgcacaactc tcacctccca acagccctct ctagtgaaca gatgtcaaga acaaactatc 1212

aaagcttcca ctttaacaaa acctgaattc tttcagagct gactctcttc tatgcctcaa 1272

aacttcagag aggaacatcc cataatgtat gccttctcat atgatattag agaggtagaa 1332

tggctcttac aactcatgta ccattgcta gttttttttt ttttaataaac gtgaaaactg 1392

agagttagat ctggtttcaa aacccaagac tgccctgattt ttagttatct ttccactatc 1452

ctaactgcct catgccctt cactagttca tgccaagaac gtgactggaa aggcatggca 1512

cctatacctt gattaatttc cattaatgga aatgggttcgt cctgagtcac ctacgttccg 1572

agtcaggctg tcactcctac ta 1594

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<211> 293

<212> PRT

<213> Homo sapiens

<400> 12

Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu Glu
1 5 10 15

Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala Phe
20 25 30

Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val Val
35 40 45

Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val Cys
50 55 60

Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr Tyr
65 70 75 80

Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly Met
85 90 95

Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe Gly
100 105 110

Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys Phe
115 120 125

Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val Ala
130 135 140

Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg Ala
145 150 155 160

Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser Leu
165 170 175

Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn Gly
180 185 190

Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met Trp
195 200 205

Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu Leu
210 215 220

Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg Leu
 225 230 235 240

Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile Gln
 245 250 255

Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu Trp Arg Ser
 260 265 270

Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met Trp Cys Gln
 275 280 285

Val Ser Ser Ser Thr
 290

<210> 13
 <211> 26
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 <213> Artificial Sequence

<220>
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 primer

<220>
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 <222> (21)
 <223> a, c, g or t

<220>
 <221> modified_base
 <222> (24)
 <223> a, c, g or t

<400> 13
 ctcacatcttcg cgggtgggcrc ngyngg

26

<210> 14
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
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 primer

<220>
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 <222> (22)
 <223> c or Inosine

<220>
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 <222> (25)
 <223> a, c, g or t

<220>
 <221> modified_base
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 <223> a, c, g or t

<400> 14
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31

<210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Degenerated
 primer

<400> 15
 gaartartag ccrcgrcagc cw

22

<210> 16
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
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 primer

<400> 16
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27

<210> 17
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 17
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23

<210> 18
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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primer

<400> 18
ggatcccaaa taagaaagg tagttgc

27

<210> 19
<211> 29
<212> DNA
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<220>
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primer

<400> 19
aaagggtagt tgcgccacat ctcataagac

29

<210> 20
<211> 29
<212> DNA
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<220>
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primer

<400> 20
aggctctatga gatgtggcgc aactaccct

29

<210> 21
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<220>
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primer

<400> 21
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30

<210> 22
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<212> DNA
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<220>
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primer

<400> 22
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<210> 23
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<212> DNA
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<220>
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primer

<400> 23
gctcagcttg aaacagagcc tcgtacc 27

<210> 24
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 24
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<210> 25
<211> 29
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
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<400> 25
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<210> 26
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 <212> DNA
 <213> Artificial Sequence

<220>
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 primer

<400> 26
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<210> 27
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
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 primer

<400> 27
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<210> 28
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 <212> DNA
 <213> Artificial Sequence

<220>
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 primer

<400> 28
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<210> 29
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 29
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<210> 30
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 <212> DNA
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<220>
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 primer

<400> 30
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<210> 31
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
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 primer

<400> 31
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<210> 32
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 32
 cctcttcagc ctggcggctct ctg 23

<210> 33
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
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 primer

<400> 33
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<210> 34
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 <212> DNA
 <213> Artificial Sequence

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 primer

 <220>
 <221> misc_binding
 <222> (1)
 <223> Labeled with 6-carboxyfluorescein

 <220>
 <221> misc_binding
 <222> (34)
 <223> Labeled with
 N,N,N',N'-tetramethyl-6-carboxyrhodamin

 <400> 34
 agatgtggcg caactaccct ttcttggtcg ggcc

34

<210> 35
 <211> 7
 <212> PRT
 <213> Unknown Organism

 <220>
 <223> Description of Unknown Organism: Illustrative
 mammalian C-terminal sequence

 <220>
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 <400> 35
 Phe Leu Phe Arg Pro Arg Asn
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